

10/554387 SEQ ID NO:8

RESULT 11
US-10-554-387-14
; Sequence 14, Application US/10554387
; Publication No. US20060204487A1
; GENERAL INFORMATION:
; APPLICANT: Shaaltiel, Yoseph
; APPLICANT: Baum, Gideon
; APPLICANT: Sharon Hashmueli
; APPLICANT: Ayala Lewkowicz
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE
; FILE REFERENCE: 30570
; CURRENT APPLICATION NUMBER: US/10/554,387
; CURRENT FILING DATE: 2005-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: High mannose human glucocerebrosidase (GCD)
US-10-554-387-14

Query Match 99.3%; Score 2648.5; DB 5; Length 526;
Best Local Similarity 99.6%; Pred. No. 1.1e-253;
Matches 495; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ARPCIPKSFQYSSVVCVNCATYCDSEDPPTFPALGTFSTRYESTRSGRRMELSMGPIQANH 60
Db 23 ARPCIPKSFQYSSVVCVNCATYCDSEDPPTFPALGTFSTRYESTRSGRRMELSMGPIQANH 82
Qy 61 TGTGLLLTLQPEQRFQKVKGFGGAMTDAAALNILALSPPAQNLLLSYFSEEGIGYNIIR 120
Db 83 TGTGLLLTLQPEQRFQKVKGFGGAMTDAAALNILALSPPAQNLLLSYFSEEGIGYNIIR 142
Qy 121 VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLASPWT 180
Db 143 VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLASPWT 202
Qy 181 SPTWLKTNQAVNGKSLKQPGDIYHQWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL 240
Db 203 SPTWLKTNQAVNGKSLKQPGDIYHQWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL 262
Qy 241 LSGYPFQCLGFTPEHQRFIARDLGPTLANSTHNVRLMLDDGRLLL-HWAKVVLTDPE 299
Db 263 LSGYPFQCLGFTPEHQRFIARDLGPTLANSTHNVRLMLDDGRLLLPHWAKVVLTDPE 322
Qy 300 AAKYVHGI AVHWYLDLFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRG 359
Db 323 AAKYVHGI AVHWYLDLFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRG 382
Qy 360 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNNWRNFVDSPIIVDITKDTFYKQPMFYHL 419
Db 383 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNNWRNFVDSPIIVDITKDTFYKQPMFYHL 442
Qy 420 GHFSKFIPEGSQRVGLVASQKNLDLDAVALMHPDGSVVVVLNRSKDVPLTIKDPVAVGFL 479
Db 443 GHFSKFIPEGSQRVGLVASQKNLDLDAVALMHPDGSVVVVLNRSKDVPLTIKDPVAVGFL 502
Qy 480 ETISPGYSIHTYLWHRQ 496
Db 503 ETISPGYSIHTYLWHRQ 519

SEQ ID NO:7

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; GENERAL INFORMATION:

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; FEATURE:
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US-10-554-387-14

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Alignment Scores:
Pred. No.:          1.48e-203      Length:           526
Score:             2673.00         Matches:          497
Percent Similarity: 100.0%         Conservative:     0
Best Local Similarity: 100.0%      Mismatches:      0
Query Match:       96.8%           Indels:           0
DB:                5               Gaps:             0

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US-10-554-387A-7 (1-1491) x US-10-554-387-14 (1-526)

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Qy      1  GCCCGCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGTGTCTGCAATGCC 60
      |||
Db      23 AlaArgProCysIleProLysSerPheGlyTyrSerSerValValCysValCysAsnAla 42

Qy      61  ACATACTGTGACTCCTTTGACCCCCGACCTTTCCTGCCCTTGGTACCTCAGCCGCTAT 120
      |||
Db      43  ThrTyrCysAspSerPheAspProProThrPheProAlaLeuGlyThrPheSerArgTyr 62

Qy      121 GAGAGTACACGCAGTGGGCGACGGATGGAGCTGAGTATGGGGCCATCCAGGTAATCAC 180
      |||
Db      63  GluSerThrArgSerGlyArgArgMetGluLeuSerMetGlyProIleGlnAlaAsnHis 82

Qy      181 ACGGGCACAGGCCTGCTACTGACCTGCAGCCAGAACAGAAGTTCAGAAAAGTGAAGGGA 240
      |||
Db      83  ThrGlyThrGlyLeuLeuLeuThrLeuGlnProGluGlnLysPheGlnLysValLysGly 102

Qy      241 TTTGGAGGGGCCATGACAGATGCTGCTCTCAACATCCTTGCCTGTACCCCTGCC 300
      |||
Db      103 PheGlyGlyAlaMetThrAspAlaAlaAlaLeuAsnIleLeuAlaLeuSerProProAla 122

Qy      301 CAAAATTTGCTACTTAAATCGTACTTCTCTGAAGAAGGAATCGGATATAACATCATCCGG 360
      |||
Db      123 GlnAsnLeuLeuLeuLysSerTyrPheSerGluGluGlyIleGlyTyrAsnIleIleArg 142

Qy      361 GTACCCATGGCCAGCTGTGACTTCTCCATCCGCACCTACACCTATGCAGACACCCTGAT 420
      |||
Db      143 ValProMetAlaSerCysAspPheSerIleArgThrTyrThrTyrAlaAspThrProAsp 162

Qy      421 GATTTCAGTTGCACAACCTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATACCCCTG 480
      |||
Db      163 AspPheGlnLeuHisAsnPheSerLeuProGluGluAspThrLysLeuLysIleProLeu 182

Qy      481 ATTCACCGAGCCCTGCAGTTGGCCAGCGTCCCGTTTCACTCCTTGCCAGCCCTGGACA 540
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Db      183 IleHisArgAlaLeuGlnLeuAlaGlnArgProValSerLeuLeuAlaSerProTrpThr 202

Qy      541 TCACCCACTTGGCTCAAGACCAATGGAGCGGTGAATGGGAAGGGGTCACTCAAGGGACAG 600
      |||
Db      203 SerProThrTrpLeuLysThrAsnGlyAlaValAsnGlyLysGlySerLeuLysGlyGln 222

Qy      601 CCCGGAGACATCTACCACCAGACCTGGGCCAGATACTTTGTGAAGTTTCCTGGATGCCTAT 660
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